RAW SEQUENCE LISTING
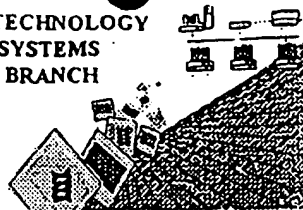## ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/733,691_

Source: _OIPE (IFWO)_

Date Processed by STIC: _12/30/03_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.1 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<u>http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm</u>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

<u>Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:</u>

1. EFS-Bio (<u><http://www.uspto.gov/ebc/efs/downloads/documents.htm></u> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
    prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
    ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
    each n or Xaa can only represent a single residue. Please present the maximum number of each
    residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
    the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for
    Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped

    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
    (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or
    is Artificial Sequence

11 ____ Use of <220>   Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
    Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or
    "Unknown." Please explain source of genetic material in <220> to <223> section.
    (See "Federal Register," 03/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 12/30/2003
PATENT APPLICATION: US/10/733,691   TIME: 11:25:40

Input Set : A:\10733691.txt
Output Set: N:\CRF4\12302003\J733691.raw

pp 1-4

```
     2 <110> APPLICANT: NIKOLICH, MIKELJON
     3         HOOVER, DAVID
     5 <120> TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS INCLUDING ROUGH PHENOTYPE BRUCELLA
HOST STRAINS
     6         AND COMPLEMENTATION DNA FRAGMENTS
     8 <130> FILE REFERENCE: ARMY 176
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/733,691
    12 <141> CURRENT FILING DATE: 2003-12-11
    14 <150> PRIOR APPLICATION NUMBER: US 60/402,164
W--> 15 US 60/533,016
    17 <151> PRIOR FILING DATE: 2002-12-12
W--> 18 2003-09-15
    20 <160> NUMBER OF SEQ ID NOS: 2
```

list these together

<150> us 60/533,016
<151> 2003-09-15

```
ERRORED SEQUENCES
```

delete *Do not insert alphabetical headings,*

Does Not Comply Corrected Diskette Needed

the CRF software will insert them.

```
E--> 23 <210> SEQ ID NO: SEQ ID NO 1
    24 <211> LENGTH: LENGTH: 2693
E--> 25 <212> TYPE: TYPE: DNA
    26 <213> ORGANISM: ORGANISM: Brucella melitensis
W--> 27 <220> FEATURE: FEATURE:
E--> 28 <400> SEQUENCE: SEQUENCE: 1
    29 caccttatgt ttgggacatt ttaattagga acgtttatgc   40
    30 cttcggatgc cgtgggcgtg gcatccgcat gagggatggc   80
    31 tttgcgtttc tgcgctttga agatgttgaa attgggttag  120
    32 ggccgcaata tggtggtgta agcctaccag catatgagtt  160
    33 tcgaaatttt gagggggttat ttcttcgccg caccgaagcc  200
    34 actggattgg atggatatac agaccttgga tacgtcccag  240
    35 atgctgaaca gcggggggttc atctttgcag acggagcagc  280
    36 cctccacatc aatagcctgt ttgcagataa taacaagggt  320
    37 gatggcgtgt tttgccaaaa cgtccaatac gtagatggaa  360
    38 acgatctcaa ttcatccatc gacggcggaa ctgggttcaa  400
    39 ttttatcaac gtagatcgca taaacatcaa tacgatccgc  440
    40 agtggtggcc gccggaatat ggcaccagga aatcttaaca  480
    41 ctgtttccca aggtatctct ttgaatgcaa attgtcagac  520
    42 tgtaattata ggcaacgcag ttacccacaa ctggtgaagt  560
    43 cacggttttt atagccaagc tcaggacatt ttggttaatg  600
    44 gtctgatatc acgtgataat ggcggaaggg ggtacgttgc  640
    45 agagggttca gcaggtcat ctctcctaaa tggggccgtt  680
    46 ttcagagata atgtagcagg gaattatttt acaggaggga  720
    47 caagcgtaaa ccatctcgcg aacttccaac ttcataactc  760
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    49 aatgggtctg cataacggtc cttgccattt taactataaa  840
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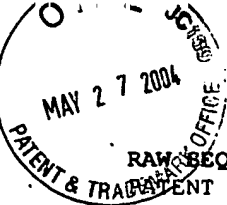
BEST AVAILABLE COPY

MAY 2 7 2004

RAW SEQUENCE LISTING   DATE: 12/30/2003
PATENT APPLICATION: US/10/733,691   TIME: 11:25:40

Input Set : A:\10733691.txt
Output Set: N:\CRF4\12302003\J733691.raw

```
50 tgagctattc ccgcgcatta agagtagaca cgggaaatca   880
51 gtatggctcc gagacatatt acagttatcc taccagctaa   920
52 gtaccgaggc ggaagtcttc gagttacgaa gaatatcgtt   960
53 cgaatgcttt tgaagggaag tcagaattat ggtgaacagt  1000
54 gtcaagttag attggcagta cgtgccgata cctacgatat  1040
55 tggggaggag tttcgtgatc ttatcgataa tggtgtagag  1080
56 gttcgggaaa tatcattcaa agaagttcct ccagaagatg  1120
57 ttaacaatgc taactatttc caaggtagaa atatcgacct  1160
58 acagtcgaga acctattggc taatggagga tggccaaaac  1200
59 aactgtgccg atagtgacct ttggctagtt gtatcctact  1240
60 ctgtagagta tcctattgcc ccgataaggc cgacactgat  1280
61 atttgccacc gatttcattc aaaggtacgt acctgatatt  1320
62 atttggccac cacggcccgg tgaggggggat gctgaggctc  1360
63 ttgcgttctt acgacaatca gacggcgtac tagctacaac  1400
64 accacacacg cygctggatg cgatttcata cgctggctta  1440
65 cctgcgtcca aagtttatct tgctccgatg gagtttgacc  1480
66 cgacgttttt ggatcgttac cggtcagtgt ctaaggttaa  1520
67 ggaaccctat ttcctttggc caaccaaccc aaatgctcac  1560
68 aaaaaccatg caaaagcgtt tcaagcgcta gacctatatt  1600
69 acggcaaact aaagggtaag ataaagacaa agatagtcgg  1640
70 tgtgagtagt gtgcggatgg acccatccca tcgatggcag  1680
71 gccaagtacg aaaataaggc ttatgtgaaa tctgtacggg  1720
72 aaattgttgc gggtctcgac aacctgaaaa gcaatgttga  1760
73 gttcgctggt gaggttgcgg acaaggagta tgcggagctt  1800
74 cttgcttcag cttgtttcct ttggcatcca actttggcag  1840
75 acaacggaac tttt gctgcg gtcgaagcgg catatatggg  1880
76 atgtccaacg ctttcaaacg actacccgca gatgcggtat  1920
77 atttctaacc gtttcgaaat tcccatgcag tattttaacg  1960
78 caaggtctgt gaaggaaatg gcatcagcgc ttaagcaaat  2000
79 ggaggagacg ccaatagatg taggtttatt gccaagtcga  2040
80 gaaaccctat ctctgcattc gtgggaagct cacgcttccg  2080
81 aatactggga tgtgatcgtg agggcagcgg catgaataag  2120
82 ctcggcgtgt ttatcggcta taacccaggc caattagatc  2160
83 catatcaggg tatttctcgc ttaattgcat tcgtgatcaa  2200
84 gggggccttg aaccagggta gcggtgtaac aattgcttgc  2240
85 cccggctggc taaaggacga tgtacgtgtt cttttggaag  2280
86 atgctgatat cccacttgaa gcggtcaaaa ttatcgcgac  2320
87 gaatggtcag cctccattgg cttcgttatg gaagttgaga  2360
88 gataagttcc gtaagagacg gacgagtaaa cgaaaacgtc  2400
89 tctggctgga gcgctatggs aaaaatgttg caaattttgt  2440
90 tgcagaatgg ctttctttgc gctcgtattg ggggattttt  2480
91 ttgggggctg ctgcaattgc tgtagtgact attctacttg  2520
92 ccgtaccaat tgctatagcc ttcaccgctc ttatcggtct  2560
93 tctatttgct cgtcggctta ttagacgtgt tatcaggtca  2600
94 aagcttggtt tgtttttttca caaaaatgcc aatcaattca  2640
95 acaaattaat gtcatctgat gaaaccatcg accggatgag  2680
96 ggaacgggaa ttc          2693
98 <210> SEQ ID NO: 2
99 <211> LENGTH: 410
```

E--> 98 <210> SEQ ID NO: (SEQ ID NO) 2
99 <211> LENGTH: (LENGTH:) 410

delete

```
E--> 100 <212> TYPE: (TYPE:) PRT
     101 <213> ORGANISM: (ORGANISM:) Brucella melitensis
E--> 102 <400> SEQUENCE: (SEQUENCE:) 2
     103 Met Ala Pro Arg His Ile Thr Val Ile Leu
E--> 104          5        10                  10
     105 Pro Ala Lys Tyr Arg Gly Gly Ser Leu Arg
E--> 106              15                 20  20
     107 Val Thr Lys Asn Ile Val Arg Met Leu Leu
E--> 108                  25               30
     109 Lys Gly Ser Gln Asn Tyr Gly Glu Gln Cys
E--> 110     35          40
     111 Gln Val Arg Leu Ala Val Arg Ala Asp Thr
E--> 112     45          50
     113 Tyr Asp Ile Gly Glu Glu Phe Arg Asp Leu
E--> 114     55          60
     116 Ile Asp Asn Gly Val Glu Val Arg Glu Ile
E--> 117     65          70
     118 Ser Phe Lys Glu Val Pro Pro Glu Asp Val
E--> 119     75          80
     120 Asn Asn Ala Asn Tyr Phe Gln Gly Arg Asn
E--> 121     85          90
     122 Ile Asp Leu Gln Ser Arg Thr Tyr Trp Leu
E--> 123     95          100
     124 Met Glu Asp Gly Gln Asn Asn Cys Ala Asp
E--> 125     105         110
     126 Ser Asp Leu Trp Leu Val Val Ser Tyr Ser
E--> 127     115         120
     128 Val Glu Tyr Pro Ile Ala Pro Ile Arg Pro
E--> 129                  125     130
     130 Thr Leu Ile Phe Ala Thr Asp Phe Ile Gln
E--> 131     135         140
     132 Arg Tyr Val Pro Asp Ile Ile Trp Pro Pro
E--> 133     145         150
     134 Arg Pro Gly Glu Gly Asp Ala Glu Ala Leu
E--> 135     155         160
     136 Ala Phe Leu Arg Gln Ser Asp Gly Val Leu
E--> 137     165         170
     138 Ala Thr Thr Pro His Thr Arg Leu Asp Ala
E--> 139     175         180
     140 Ile Ser Tyr Ala Gly Leu Pro Ala Ser Lys
E--> 141             185     190
     142 Val Tyr Leu Ala Pro Met Glu Phe Asp Pro
E--> 143             195     200
     144 Thr Phe Leu Asp Arg Tyr Arg Ser Val Ser
E--> 145     205         210
     146 Lys Val Lys Glu Pro Tyr Phe Leu Trp Pro
E--> 147     215         220
     148 Thr Asn Pro Asn Ala His Lys Asn His Ala
E--> 149     225         230
```

misaligned amino acid numbers (see item 3 on Error Summary Sheet)
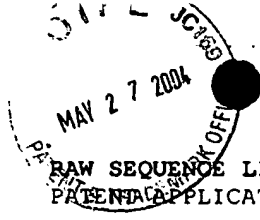
Input Set : A:\10733691.txt
Output Set: N:\CRF4\12302003\J733691.raw

```
       150 Lys Ala Phe Gln Ala Leu Asp Leu Tyr Tyr
E--> 151    235         240
       152 Gly Lys Leu Lys Gly Lys Ile Lys Thr Lys
E--> 153    245         250
      .154 Ile Val Gly Val Ser Ser Val Arg Met Asp
E--> 155    255             260
       156 Pro Ser His Arg Trp Gln Ala Lys Tyr Glu
E--> 157    265                 270
       158 Asn Lys Ala Tyr Val Lys Ser Val Arg Glu
E--> 159    275         280
       160 Ile Val Ala Gly Leu Asp Asn Leu Lys Ser
E--> 161    285         290
       162 Asn Val Glu Phe Ala Gly Glu Val Ala Asp
E--> 163    295         300
       164 Lys Glu Tyr Ala Glu Leu Leu Ala Ser Ala
E--> 165    305         310
       166 Cys Phe Leu Trp His Pro Thr Leu Ala Asp
E--> 167    315         320
       168 Asn Gly Thr Phe Ala Ala Val Glu Ala Ala
E--> 169    325         330
       170 Tyr Met Gly Cys Pro Thr Leu Ser Asn Asp
E--> 171    335         340
       172 Tyr Pro Gln Met Arg Tyr Ile Ser Asn Arg
E--> 173    345         350
       174 Phe Glu Ile Pro Met Gln Tyr Phe Asn Ala
E--> 175    355         360
       176 Arg Ser Val Lys Glu Met Ala Ser Ala Leu
E--> 177    365         370
       178 Lys Gln Met Glu Glu Thr Pro Ile Asp Val
E--> 179    375         380
       180 Gly Leu Leu Pro Ser Arg glu Thr Leu Ser
E--> 181    385         390
       182 Leu His Ser Trp Glu Ala His Ala Ser Glu
E--> 183    395         400
       184 Tyr Trp Asp Val Ile Val Arg Ala Ala Ala
E--> 185    405         410
```

VERIFICATION SUMMARY   DATE: 12/30/2003
PATENT APPLICATION: US/10/733,691   TIME: 11:25:41

Input Set : A:\10733691.txt
Output Set: N:\CRF4\12302003\J733691.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:259 W: Allowed number of lines exceeded, <150> PRIOR APPLICATION NUMBER:
L:18 M:259 W: Allowed number of lines exceeded, <151> PRIOR FILING DATE:
L:23 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:25 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:27 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:28 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:96 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:2693 SEQ:0
L:98 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:100 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:102 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQ ID NO
L:104 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:0
M:332 Repeated in SeqNo=0
L:185 M:252 E: No. of Seq. differs, <211> LENGTH:Input:0 Found:410 SEQ:0